



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 172438

TO: Chun Crowder
Location: rem/3B59/3C70
Art Unit: 1644
Thursday, December 01, 2005

Case Serial Number: 10/822300

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2005, 07:46:05 ; Search time 192 Seconds
(without alignments)
1020.640 Million cell updates/sec

Title: US-10-822-300-122XAA
Perfect score: 2372
Sequence: 1 QVQLVQSGAEVKKPQSSVKV.....LKEALNHVTKSLSPK 446

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2372	100.0	446	8	ADT51689
2	2370	99.9	446	8	ADT51687
3	2368	99.8	446	8	ADT51690
4	2366	99.7	446	8	ADT51688
5	2365	99.7	446	8	ADT51686
6	2247	94.7	465	7	ADDE4199
7	2234.5	94.2	464	2	ADUC6011
8	2233.5	94.2	652	2	AAW48650
9	2232.5	94.1	470	3	AAW90935
10	2232.5	94.1	470	5	ABW49044
11	2232	94.1	445	8	ADJ11308
12	2232	94.1	464	8	ADJ11354
13	2231.5	94.1	470	3	AAW90934
14	2231.5	94.1	470	3	ABW4903
15	2229.5	94.0	449	2	AAW43339
16	2229.5	94.0	449	2	AAW49816
17	2229.5	94.0	470	3	AAW90933
18	2229.5	94.0	470	5	ABW49032
19	2226.5	93.9	470	3	AAW93037
20	2226.5	93.9	470	3	AAW4779
21	2226.5	93.9	470	3	AAW90929
22	2226.5	93.9	470	5	ABW4944
23	2226.5	93.9	470	5	ABW4898
24	2224.5	93.8	447	8	ADT51700

25	2224.5	93.8	448	6	ABR55871	Ab-55871 Human imm
26	2224.5	93.8	448	8	ADN49728	Adn49728 Human imm
27	2224.5	93.8	448	8	ADU74404	Adu74404 Human imm
28	2223.5	93.7	449	9	ADZ80769	Adz80769 Amino aci
29	2223.5	93.7	462	3	AEBO8800	AEBO8800 Anti-NGO
30	2223.5	93.7	470	3	AAW90936	AAW90936 Humanised
31	2223.5	93.7	470	5	ABW74945	ABW74945 Humanised
32	2222.5	93.7	447	8	ADT51698	Adt51698 Humanised
33	2222	93.7	583	4	AAW83156	AAW83156 Gangliosid
34	2221.5	93.7	453	8	ADT55443	Adt55443 Anti-IGE
35	2221.5	93.7	453	9	AEBS6309	AEBS6309 Anti-IGE
36	2220.5	93.6	447	8	ADT51701	Adt51701 Fencolizum
37	2218.5	93.5	447	8	ADT51699	Adt51699 Fencolizum
38	2217.5	93.5	447	8	ADT51697	Adt51697 Fencolizum
39	2217	93.5	448	5	AAW49203	AAW49203 Humanised
40	2217	93.5	467	9	ADY30112	Ady30112 Human Igg
41	2216.5	93.4	451	8	ADR23350	ADR23350 Human CD7
42	2216	93.4	450	8	ADSL8702	Adsl8702 Protein s
43	2216	93.4	450	8	ADSL8708	Adsl8708 Protein s
44	2214.5	93.4	447	8	ADQ31274	Adq31274 Humanised
45	2214.5	93.4	447	8	ADQ31276	Adq31276 Humanised

ALIGNMENTS

RESULT 1	
ADT51689	ADT51689 strand; protein; 446 AA.
XX	XX
AC	ADT51689;
XX	XX
DT	13-JAN-2005 (first entry)
XX	XX
DE	Dacilizumab antibody gamma-1 heavy chain mutant T250Q/M428L.
XX	XX
KW	Humanised; antibody; immunoglobulin G; IgG; gamma-1 heavy chain;
KW	FcRn binding affinity; serum half-life; dacilizumab; fencolizumab;
KW	visilizumab; M200; cancer; inflammatory disorder; asthma;
KW	autoimmune disease; viral infection; cytostatic; antiinflammatory;
KW	antiallergic; immunosuppressive; virucide; mutant; mutein.
OS	Homo sapiens.
XX	XX
XX	Synthetic.
XX	XX
FT	Key
FT	Misc-difference 249
FT	Location/Qualifiers
FT	/note= "Substitution of wild-type Thr to Gln"
FT	Misc-difference 427
FT	/note= "Substitution of wild-type Met to Leu"
XX	XX
PN	WO2004092219-A2.
XX	XX
PD	28-OCT-2004.
XX	XX
PF	09-APR-2004; 2004WO-US011213.
XX	XX
PR	10-APR-2003; 2003US-0462014P.
XX	XX
PR	03-JUN-2003; 2003US-0475762P.
XX	XX
PR	29-AUG-2003; 2003US-0499048P.
XX	XX
PR	15-OCT-2003; 2003US-00687118.
XX	XX
PA	(PROT-) PROTEIN DESIGN LABS INC.
XX	XX
PI	Hinton PR, Teureshita N, Tso JY, Vaquez M;
XX	XX
DR	WPI; 2004-758341/74.
XX	XX
PT	New modified antibodies of class IgG that have altered binding affinities
XX	XX
PT	for FcRn or altered serum half-lives, useful for diagnosing or treating
XX	XX
PT	for e.g. cancer, inflammation, autoimmune diseases or viral infections.
XX	XX
PS	Claim 16; SEQ ID NO 122; 157bp; English.

XX The present invention relates to a modified human antibody of class
CC immunoglobulin G (IgG) where at least one amino acid residue from the
CC heavy chain constant (CH) region selected from amino acid residues 250,
CC 314 and 428 is different from that present in an unmodified class IGG
CC antibody, and where the FcRn binding affinity and/or serum half-life of
CC the modified antibody is altered relative to that of the unmodified
CC antibody. The numbering of the residues in the heavy chain is that of the
CC EU index. Also disclosed are methods of modifying an antibody of class
CC IGG and producing the modified antibody cited, and a pharmaceutical
CC composition comprising the above modified immunoglobulins, proteins and
CC other bioactive molecules having altered half-lives. The unmodified or
CC naturally occurring class IGG antibody is selected from daclizumab,
CC fontolizumab, visilizumab and M200. The amino acid residue 250 from the
CC heavy chain constant region is glutamic acid or glutamine, or the amino
CC acid residue 428 from the heavy chain constant region is phenylalanine or
CC leucine. Alternatively, the amino acid residue 250 from the heavy chain
CC constant region is glutamic acid and the amino acid residue 428 from the
CC heavy chain constant region is phenylalanine, or the amino acid residue
CC 250 from the heavy chain constant region is glutamine and the amino acid
CC residue 428 from the heavy chain constant region is phenylalanine, or the
CC amino acid residue 250 from the heavy chain constant region is glutamine
CC and the amino acid residue 428 from the heavy chain constant region is
CC leucine. The modified therapeutic antibody of class IGG has an in vivo
CC elimination half-life of at least 1.3-fold longer than that of the
CC of the invention are useful for various diagnostic and therapeutic
CC purposes, especially in the treatment of cancer, inflammatory disorders
CC (e.g. asthma), autoimmune diseases or viral infections. The present
CC sequence represents a mutated region of a humanised antibody. Note: The
CC position of the mutation is numbered according to the EU index.
XX
SQ Sequence 446 AA;

Query Match 100.0%; Score 2372; DB 8; Length 446;
Best Local Similarity 99.6%; Pred. No. 1.9e-133;
Matches 444; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVKKPGSSVKVCASGYSPTSRMHWRQAPQGLGWIGYINPSTGYEY 60
DB 1 QVQLVQSGAEVKKPGSSVKVCASGYSPTSRMHWRQAPQGLGWIGYINPSTGYEY 60
QY 61 NQKFKDKATITADESTNTAYMELSLRSRSDTAVYTCARGGGVFDYWGQTLTVSSASTK 120
DB 61 NQKFKDKATITADESTNTAYMELSLRSRSDTAVYTCARGGGVFDYWGQTLTVSSASTK 120
QY 121 GPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
DB 121 GPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
QY 181 LGSVTVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPCPAPPELLGGPSVF 240
DB 181 LGSVTVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTHTCPPCPAPPELLGGPSVF 240
QY 241 LFPFKPKDQMIKSRTEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYR 300
DB 241 LFPFKPKDQMIKSRTEVTCVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYR 300
QY 301 VSVLTIVLHVDWLNKGEYKCKVSNKALPAPIETKISKAKGPQEPQVYTLPPSRDELTKN 360
DB 301 VSVLTIVLHVDWLNKGEYKCKVSNKALPAPIETKISKAKGPQEPQVYTLPPSRDELTKN 360
QY 361 QVSLTCLVKGFPYSDTAVESNGQPENNYKTPPVLDSDGGSFYSLKLTVDKSRWQQGN 420
DB 361 QVSLTCLVKGFPYSDTAVESNGQPENNYKTPPVLDSDGGSFYSLKLTVDKSRWQQGN 420
QY 421 VFSCSVLKEALHNHYTKQSLSPGK 446
DB 421 VFSCSVLKEALHNHYTKQSLSPGK 446

RESULT 2
ADT51687

ID ADT51687 standard; protein; 446 AA.
XX
AC ADT51687;
XX
DT 13-JAN-2005 (first entry)
XX
DE Daclizumab antibody gamma-1 heavy chain mutant T250Q.
XX
KW Humanised; antibody; immunoglobulin G; IGG; gamma-1 heavy chain;
KW FcRn binding affinity; serum half-life; daclizumab; fontolizumab;
KW visilizumab; M200; cancer; inflammatory disorder; asthma;
KW autoimmune disease; viral infection; cytostatic; antiinflammatory;
KW antiasthmatic; immunosuppressive; virucide; mutant; mutein.
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 249 /note= "Substitution of wild-type Thr to Gln"
FT
FT
XX
XX W02004092219-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US011213.
XX
XX 10-APR-2003; 2003US-0462014P.
XX 03-JUN-2003; 2003US-0475762P.
XX 29-AUG-2003; 2003US-0499048P.
XX 15-OCT-2003; 2003US-00687118.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Hinton PR, Tsurushita N, Tso JY, Vasquez M;
XX WPI; 2004-758341/74.
XX
XX New modified antibodies of class IGG that have altered binding affinities
XX for FcRn or altered serum half-lives, useful for diagnosing or treating
XX for e.g. cancer, inflammation, autoimmune diseases or viral infections.
XX
XX Claim 16; SEQ ID NO 120; 157pp; English.
XX
XX The present invention relates to a modified human antibody of class
XX immunoglobulin G (IgG) where at least one amino acid residue from the
XX heavy chain constant (CH) region selected from amino acid residues 250,
XX 314 and 428 is different from that present in an unmodified class IGG
XX antibody, and where the FcRn binding affinity and/or serum half-life of
XX the modified antibody is altered relative to that of the unmodified
XX antibody. The numbering of the residues in the heavy chain is that of the
XX EU index. Also disclosed are methods of modifying an antibody of class
XX IGG and producing the modified antibody cited, and a pharmaceutical
XX composition comprising the above modified immunoglobulins, proteins and
XX other bioactive molecules having altered half-lives. The unmodified or
XX naturally occurring class IGG antibody is selected from daclizumab,
XX fontolizumab, visilizumab and M200. The amino acid residue 250 from the
XX heavy chain constant region is glutamic acid or glutamine, or the amino
XX acid residue 428 from the heavy chain constant region is phenylalanine or
XX leucine. Alternatively, the amino acid residue 250 from the heavy chain
XX constant region is glutamic acid and the amino acid residue 428 from the
XX heavy chain constant region is phenylalanine, or the amino acid residue
XX 250 from the heavy chain constant region is glutamine and the amino acid
XX residue 428 from the heavy chain constant region is phenylalanine, or the
XX amino acid residue 250 from the heavy chain constant region is glutamine
XX and the amino acid residue 428 from the heavy chain constant region is
XX leucine. The modified therapeutic antibody of class IGG has an in vivo
XX elimination half-life of at least 1.3-fold longer than that of the
XX corresponding unmodified class IGG antibody. The composition and methods
XX of the invention are useful for various diagnostic and therapeutic
XX purposes, especially in the treatment of cancer, inflammatory disorders
XX (e.g. asthma), autoimmune diseases or viral infections. The present
XX sequence represents a mutated region of a humanised antibody. Note: The
XX

GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: December 1, 2005, 07:54:27 ; Search time 45 Seconds
(without alignments)
819.408 Million cell updates/sec

Title: US-10-822-300-122XAA

Perfect score: 2372

Sequence: 1 QVQLVQSGAEVKKPGSSVKV.....LKEALHNYTKSLISLSPGK 446

Scoring table: BLOSUM62DX

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents, AA:*

1: /cgn2_6/prodata/1/1aa/5 COMB.pep:.*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep:.*
3: /cgn2_6/prodata/1/1aa/H COMB.pep:.*
4: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/RE COMB.pep:.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2229.5	94.0	449	1 US-08-458-516-13	Sequence 13, Appl
2	2192.5	92.4	472	2 US-09-301-593-43	Sequence 43, Appl
3	2180.5	91.9	470	2 US-09-338-741-4	Sequence 4, Appl
4	2168	91.4	452	2 US-09-027-449-71	Sequence 71, Appl
5	2168	91.4	452	2 US-09-026-985-71	Sequence 71, Appl
6	2168	91.4	452	2 US-09-121-952A-71	Sequence 71, Appl
7	2168	91.4	452	2 US-09-234-340A-71	Sequence 71, Appl
8	2168	91.4	452	2 US-09-355-014-71	Sequence 71, Appl
9	2161.5	91.1	489	1 US-08-378-939-10	Sequence 10, Appl
10	2155	90.9	479	2 US-10-104-047-3329	Sequence 3329, Ap
11	2143	90.3	454	1 US-07-834-373C-22	Sequence 22, Appl
12	2143	90.3	454	2 US-08-437-642B-22	Sequence 22, Appl
13	2143	90.3	454	2 US-08-146-206C-22	Sequence 22, Appl
14	2143	90.3	454	2 US-09-705-686-22	Sequence 22, Appl
15	2143	90.3	454	2 US-09-705-392A-22	Sequence 22, Appl
16	2143	90.3	454	2 US-09-705-398-22	Sequence 22, Appl
17	2143	90.3	454	4 PCT-US93-07832-22	Sequence 22, Appl
18	2140	90.2	453	2 US-09-301-593-18	Sequence 18, Appl
19	2134.5	90.0	466	2 US-09-698-705-11	Sequence 11, Appl
20	2131.5	89.9	468	2 US-09-485-737B-67	Sequence 67, Appl
21	2131.5	89.9	468	2 US-10-071-485-67	Sequence 67, Appl
22	2131.5	89.9	711	2 US-09-485-737B-90	Sequence 90, Appl
23	2131.5	89.9	711	2 US-10-071-485-90	Sequence 90, Appl
24	2127.5	89.7	472	2 US-09-301-593-30	Sequence 30, Appl
25	2123	89.5	467	2 US-09-049-672A-8	Sequence 8, Appl
26	2113	89.1	449	2 US-09-679-397-2	Sequence 2, Appl
27	2113	89.1	449	2 US-09-680-148-2	Sequence 2, Appl

28	2113	89.1	449	2 US-09-304-465A-2	Sequence 2, Appl
29	2113	89.1	449	2 US-10-356-974-2	Sequence 2, Appl
30	2102.5	88.6	451	2 US-09-247-352-3	Sequence 3, Appl
31	2102.5	88.6	451	2 US-09-466-635-3	Sequence 3, Appl
32	2093.5	88.3	478	2 US-08-487-550-8	Sequence 8, Appl
33	2093.5	88.3	478	2 US-09-526-098-8	Sequence 8, Appl
34	2093.5	88.3	478	2 US-09-383-916-8	Sequence 8, Appl
35	2093.5	88.3	478	2 US-09-758-173-8	Sequence 8, Appl
36	2093.5	88.3	478	2 US-09-576-424-8	Sequence 8, Appl
37	2084.5	87.9	451	1 US-08-887-352B-18	Sequence 18, Appl
38	2084.5	87.9	451	2 US-09-109-207C-18	Sequence 18, Appl
39	2084.5	87.9	451	2 US-09-282-505-2	Sequence 2, Appl
40	2084.5	87.9	451	2 US-09-034-255-2	Sequence 2, Appl
41	2084.5	87.9	451	2 US-09-296-005-18	Sequence 18, Appl
42	2084.5	87.9	451	2 US-09-282-846-2	Sequence 2, Appl
43	2084.5	87.9	451	2 US-09-680-145-2	Sequence 2, Appl
44	2084.5	87.9	451	2 US-09-920-171-18	Sequence 18, Appl
45	2084.5	87.9	451	2 US-09-716-028-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIb/IIIa
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESS: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 94.0%; Score 2229.5; DB 1; Length 449;
Best Local Similarity 93.5%; Pred. No. 5e-162;
Matches 420; Conservative 10; Mismatches 16; Indels 3; Gaps 1;
QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYRMHWVQAPGQGLEWIGYINPSTGYTEY 60

Db 1 QVQLVQSGAEVKPGSSVKVSKASGYFTNYLIEWVRQAPGQGLEWIGVYPCSGGTNY 60
QY 61 NQKPKDKATITADSTNTAYMELSLRSEDFAVYYCAR---GGVFDYWGQGLTVTVSSA 117
Db 61 NEKPKGRVTLTVDSSTNTAYMELSLRSEDFAVYFCARRDNGYGMFAYWGQGLTVTVSSA 120
QY 118 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPPVPTVSNWNSGALTSGVHTFPAVLQSSG 177
Db 121 STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPPVPTVSNWNSGALTSGVHTFPAVLQSSG 180
QY 178 LYSLSVVTVPSLSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPPELLGGP 237
Db 181 LYSLSVVTVPSLSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPPELLGGP 240
QY 238 SVFLPPPKPKDOXMIKSRTPETCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREQYNS 297
Db 241 SVFLPPPKPKDOLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREQYNS 300
QY 298 TYRVVSVLTVLHQDLWNGKEYCKKVSNAKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 357
Db 301 TYRVVSVLTVLHQDLWNGKEYCKKVSNAKALPAPIEKTISKAKGQPRPQVYTLPPSRDEL 360
QY 358 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 417
Db 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 420
QY 418 QGNVFPSCVLEALHNHYTQKSLSLSPGK 446
Db 421 QGNVFPSCVMEALHNHYTQKSLSLSPGK 449

RESULT 2

US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.189001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-43

Query Match 92.4%; Score 2192.5; DB 2; Length 472;
Best Local Similarity 91.2%; Pred. No. 3.5e-159;
Matches 414; Conservative 12; Mismatches 19; Indels 9; Gaps 2;

QY 1 QVQLVQSGAEVKPGSSVKVSKASGYFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
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QY 61 NQKPKDKATITADSTNTAYMELSLRSEDFAVYYCAR-----GGVFDYWGQGLTV 112
Db 80 NQKPKGRVTLTVGKASATAYMELSLRSEDFAVYFCARRIAYGVDEGHANDYWGQGLTV 139
QY 113 TVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPPVPTVSNWNSGALTSGVHTFPAV 172

Db 140 TVSS-STKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPPVPTVSNWNSGALTSGVHTFPAV 198
QY 173 LOSSGLYSLSSVVTVPSLSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPE 232
Db 199 LOSSGLYSLSSVVTVPSLSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPE 258
QY 233 LLGGPSVFLPPPKPKDOXMIKSRTPETCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRE 292
Db 259 LLGGPSVFLPPPKPKDOLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPRE 318
QY 293 EQNSTYRVVSVLTVLHQDLWNGKEYCKKVSNAKALPAPIEKTISKAKGQPRPQVYTLPP 352
Db 319 EQNSTYRVVSVLTVLHQDLWNGKEYCKKVSNAKALPAPIEKTISKAKGQPRPQVYTLPP 378
QY 353 SRDELTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 412
Db 379 SREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 438
QY 413 KSRWQGNVFPSCVLEALHNHYTQKSLSLSPGK 446
Db 439 KSRWQGNVFPSCVMEALHNHYTQKSLSLSPGK 472

RESULT 3

US-09-238-741-4
; Sequence 4, Application US/09238741
; Patent No. 6897044
; GENERAL INFORMATION:
; APPLICANT: BRASLAWSKI, GARY R.
; APPLICANT: HANNA, NABIL
; APPLICANT: HARIHARAN, KANDASAMY
; APPLICANT: LABARRE, MICHAEL J.
; APPLICANT: HUYNH, TRI B.
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
; FILE REFERENCE: 23522.0584
; CURRENT APPLICATION NUMBER: US/09/238,741
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-09-238-741-4

Query Match 91.9%; Score 2180.5; DB 2; Length 470;
Best Local Similarity 90.7%; Pred. No. 2.9e-158;
Matches 409; Conservative 16; Mismatches 21; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVKPGSSVKVSKASGYFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
Db 20 QVQLVQSGAEVLKPGASVVRMSCKASGYFTSYNMHWVKQTGPGLEWIGALYIPGNGDTSY 79
QY 61 NQKPKDKATITADSTNTAYMELSLRSEDFAVYYCAR-----GGVFDYWGQGLTVTVS 115
Db 80 NQKPKGRVTLTVADKSSSTAYMQLSSLTSDSAVYYCARSTYGGDWYFNWVGAGITTVTVS 139
QY 116 SASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPPVPTVSNWNSGALTSGVHTFPAVLQ 175
Db 140 AASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPPVPTVSNWNSGALTSGVHTFPAVLQ 199
QY 176 SGLYSLSVVTVPSLSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPPELLG 235
Db 200 SGLYSLSVVTVPSLSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPPELLG 259
QY 236 GPSVFLPPPKPKDOXMIKSRTPETCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREQY 295
Db 260 GPSVFLPPPKPKDOLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREQY 319
QY 296 NSTYRVVSVLTVLHQDLWNGKEYCKKVSNAKALPAPIEKTISKAKGQPRPQVYTLPPSRD 355

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OM protein - protein search, using sw model

Run on: December 1, 2005, 07:49:39 ; Search time 165 Seconds

(without alignments)
1129.405 Million cell updates/sec

Title: US-10-822-300-122XAA

Sequence: 1 QVQLVQSGAEVKKPSSSVKRV.....LAEALHNYTKSLSPGK 446

Scoring table: BLOSUM62DX

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodataa1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodataa1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodataa1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodataa1/pubppaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/prodataa1/pubppaa/US10_PUBCOMB.pep:*
- 6: /cgn2_6/prodataa1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2372	100.0	446	5	US-10-822-300-122 Sequence 122, App
2	2370	99.9	446	5	US-10-822-300-120 Sequence 120, App
3	2368	99.8	446	5	US-10-822-300-123 Sequence 123, App
4	2366	99.7	446	5	US-10-822-300-121 Sequence 121, App
5	2365	99.7	446	5	US-10-822-300-119 Sequence 119, App
6	2364	99.7	446	5	US-10-822-300-117 Sequence 117, App
7	2332.5	94.1	470	4	US-10-822-300-147 Sequence 147, App
8	2332.5	94.1	470	4	US-10-822-300-145 Sequence 145, App
9	2331.5	94.1	470	4	US-10-822-300-143 Sequence 143, App
10	2331.5	94.1	470	4	US-10-822-300-141 Sequence 141, App
11	2329.5	94.0	470	4	US-10-822-300-139 Sequence 139, App
12	2329.5	94.0	470	4	US-10-822-300-137 Sequence 137, App
13	2326.5	93.9	470	4	US-10-822-300-135 Sequence 135, App
14	2326.5	93.9	470	4	US-10-822-300-133 Sequence 133, App
15	2324.5	93.8	448	4	US-10-822-300-131 Sequence 131, App
16	2324.5	93.8	448	4	US-10-822-300-129 Sequence 129, App
17	2324.5	93.8	448	4	US-10-822-300-127 Sequence 127, App
18	2324.5	93.8	448	4	US-10-822-300-125 Sequence 125, App
19	2324.5	93.8	448	4	US-10-822-300-123 Sequence 123, App
20	2324.5	93.8	448	4	US-10-822-300-121 Sequence 121, App
21	2324.5	93.8	448	4	US-10-822-300-119 Sequence 119, App
22	2324.5	93.8	448	4	US-10-822-300-117 Sequence 117, App
23	2324.5	93.8	448	4	US-10-822-300-115 Sequence 115, App
24	2324.5	93.8	448	4	US-10-822-300-113 Sequence 113, App
25	2324.5	93.8	448	4	US-10-822-300-111 Sequence 111, App
26	2324.5	93.8	448	4	US-10-822-300-109 Sequence 109, App
27	2324.5	93.8	448	4	US-10-822-300-107 Sequence 107, App

28	2223.5	93.7	470	4	US-10-216-484-157 Sequence 157, App
29	2223.5	93.7	470	4	US-10-216-484-155 Sequence 155, App
30	2223.5	93.7	447	5	US-10-822-300-131 Sequence 131, App
31	2221.5	93.7	453	6	US-10-813-483-6 Sequence 6, Appl1
32	2221.5	93.7	453	6	US-10-813-483-6 Sequence 6, Appl1
33	2220.5	93.6	447	5	US-10-822-300-134 Sequence 134, App
34	2218.5	93.5	447	5	US-10-822-300-132 Sequence 132, App
35	2217.5	93.5	447	5	US-10-822-300-130 Sequence 130, App
36	2217	93.5	448	4	US-10-378-567-2 Sequence 2, Appl1
37	2213.5	93.3	470	4	US-10-216-484-89 Sequence 89, Appl1
38	2213.5	93.3	470	4	US-10-216-484-89 Sequence 89, Appl1
39	2205	93.0	465	5	US-10-404-724-25 Sequence 25, Appl1
40	2205	93.0	465	5	US-10-816-276-21 Sequence 21, Appl1
41	2204	92.9	731	3	US-09-825-012-46 Sequence 46, Appl1
42	2204	92.9	741	3	US-09-825-012-55 Sequence 55, Appl1
43	2202	92.8	448	4	US-10-171-452A-48 Sequence 48, Appl1
44	2202	92.8	448	4	US-10-171-452A-60 Sequence 60, Appl1
45	2202	92.8	448	4	US-10-353-708-48 Sequence 48, Appl1

ALIGNMENTS

RESULT 1									
US-10-822-300-122									
Sequence 122, Application US/10822300									
Publication No. US20050014934A1									
GENERAL INFORMATION:									
APPLICANT: Hinton, et al.									
TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF									
FILE REFERENCE: 05882, 0039, CPUS01									
CURRENT APPLICATION NUMBER: US/10/822, 300									
CURRENT FILING DATE: 2004-04-09									
NUMBER OF SEQ ID NOS: 146									
SOFTWARE: PatentIn version 3.2									
SEQ ID NO 122									
LENGTH: 446									
TYPE: PR									
ORGANISM: Homo sapiens									
US-10-822-300-122									
Query Match									
Best Local Similarity 99.6%; Pred. No. 9.4e-146;									
Matches 444; Conservative 2; Mismatches 0; Indels 0; Gaps 0;									
QY	1	QVQLVQSGAEVKKPSSSVKSCASGYFTFYMHWVQADGGLEWIGYINPSGYTEY	60						
DB	1	QVQLVQSGAEVKKPSSSVKSCASGYFTFYMHWVQADGGLEWIGYINPSGYTEY	60						
QY	61	NKPFQKATITADESTNAYVELSLRSEDTAVVYCAAGGVFDYWGQGLVTVSSASTK	120						
DB	61	NKPFQKATITADESTNAYVELSLRSEDTAVVYCAAGGVFDYWGQGLVTVSSASTK	120						
QY	121	GSVPEPLAPSSKSTSGTALGCLVQDYFPBPVTVSNMAGLTSQVHTPPAVLQSSGLYS	180						
DB	121	GSVPEPLAPSSKSTSGTALGCLVQDYFPBPVTVSNMAGLTSQVHTPPAVLQSSGLYS	180						
QY	181	LSVTVTVSSLSGTQTYICNNVHKPSNKKVKKPKSCDKTHCPCPAPELIGGPAVF	240						
DB	181	LSVTVTVSSLSGTQTYICNNVHKPSNKKVKKPKSCDKTHCPCPAPELIGGPAVF	240						
QY	241	LFPPKPKQGLMSRPEVTVGVVSHDPEVKFMVYDGVVHNAKTKPREEQNSTYR	300						
DB	241	LFPPKPKQGLMSRPEVTVGVVSHDPEVKFMVYDGVVHNAKTKPREEQNSTYR	300						
QY	301	VVSIVTLVTHQDLNKEIKYKSNKALPAPLEKITSKAKGPREQVYTLPPSRDELTKN	360						
DB	301	VVSIVTLVTHQDLNKEIKYKSNKALPAPLEKITSKAKGPREQVYTLPPSRDELTKN	360						
QY	361	QVSLCLVKGFPSPDIAYVWESNGQPRENNYKTPPVLDSDGSFFLYSKLTVYDKSMOON	420						
DB	361	QVSLCLVKGFPSPDIAYVWESNGQPRENNYKTPPVLDSDGSFFLYSKLTVYDKSMOON	420						

QY 421 VFSCSVLXKALHNNHYTKSLSPGK 446
DB 421 VFSCSVLXKALHNNHYTKSLSPGK 446

RESULT 2

US-10-822-300-120
; Sequence 120, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-120

Query Match 99.9%; Score 2370; DB 5; Length 446;
Best Local Similarity 99.3%; Pred. No. 1.3e-145; Indels 0; Gaps 0;
Matches 443; Conservative 3; Mismatches 0;

QY 1 QVQLVQSGAEVKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
DB 1 QVQLVQSGAEVKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARGGVFDYWGQGLTVTVSSASTK 120
DB 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARGGVFDYWGQGLTVTVSSASTK 120
QY 121 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
DB 121 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
QY 181 LSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHTCCPCPAPPELLGGPSVF 240
DB 181 LSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHTCCPCPAPPELLGGPSVF 240
QY 241 LFPPKPKDQKXIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 300
DB 241 LFPPKPKDQKXIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 300
QY 301 VVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 360
DB 301 VVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 360
QY 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQOQN 420
DB 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQOQN 420
QY 421 VFSCSVLXKALHNNHYTKSLSPGK 446
DB 421 VFSCSVLXKALHNNHYTKSLSPGK 446

RESULT 3

US-10-822-300-123
; Sequence 123, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09

; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-123

Query Match 99.8%; Score 2368; DB 5; Length 446;
Best Local Similarity 99.3%; Pred. No. 1.7e-145; Indels 0; Gaps 0;
Matches 443; Conservative 2; Mismatches 1;

QY 1 QVQLVQSGAEVKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
DB 1 QVQLVQSGAEVKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARGGVFDYWGQGLTVTVSSASTK 120
DB 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARGGVFDYWGQGLTVTVSSASTK 120
QY 121 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
DB 121 GPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 180
QY 181 LSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHTCCPCPAPPELLGGPSVF 240
DB 181 LSSVVTVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHTCCPCPAPPELLGGPSVF 240
QY 241 LFPPKPKDQKXIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 300
DB 241 LFPPKPKDQKXIMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 300
QY 301 VVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 360
DB 301 VVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDELTKN 360
QY 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQOQN 420
DB 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQOQN 420
QY 421 VFSCSVLXKALHNNHYTKSLSPGK 446
DB 421 VFSCSVLXKALHNNHYTKSLSPGK 446

RESULT 4

US-10-822-300-121
; Sequence 121, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 121
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-121

Query Match 99.7%; Score 2366; DB 5; Length 446;
Best Local Similarity 99.3%; Pred. No. 2.3e-145; Indels 0; Gaps 0;
Matches 443; Conservative 2; Mismatches 1;

QY 1 QVQLVQSGAEVKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
DB 1 QVQLVQSGAEVKPKGSSVKVSKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
QY 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARGGVFDYWGQGLTVTVSSASTK 120

QY 301 VSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREQVYTLPPSRDELTKN 360
DB 301 VSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREQVYTLPPSRDELTKN 360
QY 361 QVSLTCLVKGFPSPDIAVEWESNGQPNENYKTPPVLDSDGSPFLYSLKLTVDKSRWQGN 420
DB 361 QVSLTCLVKGFPSPDIAVEWESNGQPNENYKTPPVLDSDGSPFLYSLKLTVDKSRWQGN 420
QY 421 VFSCSVLKEALHNNHYTKSLSPGK 446
DB 421 VFSCSVLKEALHNNHYTKSLSPGK 446

RESULT 2
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6

Query Match 89.0%; Score 2111; DB 7; Length 444;
Best Local Similarity 88.1%; Pred. No. 3.8e-130;
Matches 393; Conservative 24; Mismatches 27; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVKKPGSSVKVCCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGYTEY 60
DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSSYDMSWVRQAPGKGLIEWVSTISSGGSVYY 60
QY 61 NQKPKDKATITADESTNTAYMELSLRSEDVAVYCARGGVFDYWGOGTLTVTSSASTK 120
DB 61 LDSIKGRFTIRDNNAKSLYLQMSLRADETAVYCARQG--LDYWGRTLTVTSSASTK 118
QY 121 GPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYS 180
DB 119 GPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYS 178
QY 181 LSSVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHCTCPCPAPPELLGGPSVF 240
DB 179 LSSVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHCTCPCPAPPELLGGPSVF 238
QY 241 LPPPKPKDQXMIKSRPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 300
DB 239 LPPPKPKDQXMIKSRPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 298
QY 301 VSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREQVYTLPPSRDELTKN 360
DB 299 VSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREQVYTLPPSRDELTKN 358
QY 361 QVSLTCLVKGFPSPDIAVEWESNGQPNENYKTPPVLDSDGSPFLYSLKLTVDKSRWQGN 420

DB 359 QVSLTCLVKGFPSPDIAVEWESNGQPNENYKTPPVLDSDGSPFLYSLKLTVDKSRWQGN 418
QY 421 VFSCSVLKEALHNNHYTKSLSPGK 446
DB 419 VFSCSVLKEALHNNHYTKSLSPGK 444

RESULT 3
US-11-139-499-8
; Sequence 8, Application US/11139499
; Publication No. US20050260205A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: BRAMS, PETER
; APPLICANT: HEARD, CHERYL
; TITLE OF INVENTION: INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
; TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
; FILE REFERENCE: 37003-275681
; CURRENT APPLICATION NUMBER: US/11/139,499
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/09/576,424
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US97/19906
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 08/746,361
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: 08/487,550
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-139-499-8

Query Match 88.3%; Score 2093.5; DB 7; Length 478;
Best Local Similarity 85.4%; Pred. No. 5.5e-129;
Matches 392; Conservative 27; Mismatches 27; Indels 13; Gaps 3;

QY 1 QVQLVQSGAEVKKPGSSVKVCCKASGYTFTSYRMHWVRQAPGQGLEWIGYI--NPSTGYT 58
DB 20 EVQLVESGGGLVQPGSLRSCAVSGFTFSDHYMYWFRQAPGKPEWGFIRNKNGGTT 79
QY 59 EYNQKFKDKATITADESTNTAYMELSLRSEDVAVYIC-----ARG----GGVFDYWG 107
DB 80 EYAAVKDRFTISRDSDKSIINVLQMSLKIEDTAVYICTSYISHCRGGVCGYGFEPWG 139
QY 108 QGTLVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVH 167
DB 140 QGALVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVH 199
QY 168 TFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHCTCP 227
DB 200 TFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHCTCP 259
QY 228 CPAPPELLGGPSVFLPPKPKDQXMIKSRPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 287
DB 260 CPAPPELLGGPSVFLPPKPKDQXMIKSRPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK 319
QY 288 TKPREEQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREQV 347
DB 320 TKPREEQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREQV 379
QY 348 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPNENYKTPPVLDSDGSPFLYS 407
DB 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPNENYKTPPVLDSDGSPFLYS 439
QY 408 KLTVDKSRWQGNVFCSSVLKEALHNNHYTKSLSPGK 446
DB 440 KLTVDKSRWQGNVFCSSVLKEALHNNHYTKSLSPGK 478

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2005, 07:46:08 ; Search time 229 Seconds
(without alignments)
1374.086 Million cell updates/sec

Title: US-10-822-300-122XAA
Perfect score: 2372
Sequence: 1 QV0LV0SGAEVKKKPGSSVKV.....LKEALHNHYTQKSLSLSPGK 446

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_05.80.*
1: uniprot_prot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2152	90.7	469	2 Q727P5_HUMAN	Q727P5 homo sapien
2	2138.5	90.2	469	2 Q6PUJ1_HUMAN	Q6PUJ1 homo sapien
3	2124	89.5	475	2 Q6N095_HUMAN	Q6N095 homo sapien
4	2117	89.2	469	2 Q569P4_HUMAN	Q569P4 homo sapien
5	2083.5	87.8	466	2 Q6N096_HUMAN	Q6N096 homo sapien
6	2081.5	87.8	470	2 Q6PUJ4_HUMAN	Q6PUJ4 homo sapien
7	2081.5	87.8	480	2 Q6N094_HUMAN	Q6N094 homo sapien
8	2076.5	87.5	472	2 Q6N089_HUMAN	Q6N089 homo sapien
9	2076	87.5	475	2 Q5EPE5_HUMAN	Q5EPE5 homo sapien
10	2074	87.4	473	2 Q6MZV7_HUMAN	Q6MZV7 homo sapien
11	2074	87.4	475	2 Q6MZ06_HUMAN	Q6MZ06 homo sapien
12	2071.5	87.3	466	2 Q6IN78_HUMAN	Q6IN78 homo sapien
13	2055	86.6	544	2 Q6PJ95_HUMAN	Q6PJ95 homo sapien
14	2053.5	86.6	470	2 Q7Z5V1_HUMAN	Q7Z5V1 homo sapien
15	2049.5	86.4	478	2 Q6PI81_HUMAN	Q6PI81 homo sapien
16	2047	86.3	473	2 Q6P055_HUMAN	Q6P055 homo sapien
17	2047	86.3	475	2 Q6GMW7_HUMAN	Q6GMW7 homo sapien
18	2045.5	86.2	518	2 Q6N030_HUMAN	Q6N030 homo sapien
19	2043	86.1	465	2 Q6GMX6_HUMAN	Q6GMX6 homo sapien
20	2034	85.8	475	2 Q5RE17_PONPY	Q5RE17 pongo pygma
21	2023.5	85.3	476	2 Q6GMK1_HUMAN	Q6GMK1 homo sapien
22	2023	85.3	481	2 Q6N097_HUMAN	Q6N097 homo sapien
23	2022	85.2	519	2 Q5EBH2_HUMAN	Q5EBH2 homo sapien
24	2019.5	85.1	482	2 Q7Z351_HUMAN	Q7Z351 homo sapien
25	1919.5	80.9	464	2 Q6MZ06_HUMAN	Q6MZ06 homo sapien
26	1899	80.1	455	2 Q6PGC4_HUMAN	Q6PGC4 homo sapien
27	1897	80.0	521	2 Q8N4Y9_HUMAN	Q8N4Y9 homo sapien
28	1885.5	79.5	470	2 Q6N093_HUMAN	Q6N093 homo sapien
29	1843.5	77.7	417	2 Q6N093_HUMAN	Q6N093 homo sapien
30	1820.5	76.7	473	2 Q8TC63_HUMAN	Q8TC63 homo sapien
31	1797	75.8	348	2 Q6PYX1_HUMAN	Q6PYX1 homo sapien

32	1796	75.7	476	2 Q6MZX7_HUMAN	Q6MZX7 homo sapien
33	1748	73.7	330	1 IGHG1_HUMAN	P01857 homo sapien
34	1603	67.6	487	2 Q65ZL2_SMURI	Q65ZL2 mus sp. fv/
35	1597.5	67.3	509	2 Q8NF17_HUMAN	Q8NF17 homo sapien
36	1595	66.8	326	1 IGHG2_HUMAN	P01859 homo sapien
37	1574	66.4	465	2 Q6PUB2_MOUSE	Q6PUB2 mus musculu
38	1571.5	66.3	327	1 IGHG4_HUMAN	P01861 mus musculu
39	1571	66.2	473	2 Q9DBL4_MOUSE	Q9DBL4 mus musculu
40	1560.5	65.8	468	2 Q569W9_MOUSE	Q569W9 mus musculu
41	1557.5	65.7	470	2 Q7TMC1_MOUSE	Q7TMC1 mus musculu
42	1554	65.5	463	2 Q9PLC4_MOUSE	Q9PLC4 mus musculu
43	1544.5	65.1	458	2 Q5BJ22_RAT	Q5BJ22 rattus norv
44	1529.5	64.5	472	2 Q5BJA7_MOUSE	Q5BJA7 mus musculu
45	1527.5	64.4	468	2 Q505N9_MOUSE	Q505N9 mus musculu

ALIGNMENTS

RESULT 1
Q727P5_HUMAN PRELIMINARY; PRT; 469 AA.
ID Q727P5_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lottelino N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Buterfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (Apr-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC051328; AAH51328.1; -, mRNA.
DR HSSP, P01857; IGH1.
DR SMR, Q727P5; 20-469.
DR InterPro, IPR007110; IG_1like.
DR InterPro, IPR003597; IG_C1.
DR InterPro, IPR003066; IG_MHC.
DR InterPro, IPR003596; IG_V.
DR Pfam, PF07654; C1-sect; 3.
DR SMART, SM00406; IGV; 1.
DR PROSITE, PS50835; IG_LIKE; 4.
DR PROSITE, PS00290; IG_MHC; UNKNOWN_2.

KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
Query Match 90.7%; Score 2152; DB 2; Length 469;
Best Local Similarity 90.0%; Pred. No. 2.1e-135;
Matches 405; Conservative 19; Mismatches 22; Indels 4; Gaps 2;
QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGVTEY 60
DB 20 QVHLVQSGAEVKKPGASVKLSCKTSGYNFSYDLIWRQAPGQGLEWGWISAHNGDTKY 79
QY 61 NQKFKDKATITADESTNTAYMELSLRSEDYAVYCA---RGG-GVFDYWGQGLTVTVSS 116
DB 80 ARKFGQGRVTMTDTSATTSYMEFRSLRSDTALFYCATKSRGQGVGDFDSWGQGLTVTVSS 139
QY 117 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 176
DB 140 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 199
QY 177 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSNITKVDKVEPKSCDKTHTCPCPAPPELLGG 236
DB 200 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSNITKVDKVEPKSCDKTHTCPCPAPPELLGG 259
QY 237 PSVFLFPPKPKDQXMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296
DB 260 PSVFLFPPKPKDQXMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 319
QY 297 STYRVSVLVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 356
DB 320 STYRVSVLVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 379
QY 357 LFNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 416
DB 380 LFNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 439
QY 417 QQGNVFCVSVLXALHNHYTQKSLSLSPGK 446
DB 440 QQGNVFCVSVLXALHNHYTQKSLSLSPGK 469
RESULT 2
Q6PJF1_HUMAN PRELIMINARY; PRT; 480 AA.
ID Q6PJF1_HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6PJF1.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullhly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2].
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC016381; AAH16381.1; -; mRNA.
DR HSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;
Query Match 90.2%; Score 2138.5; DB 2; Length 480;
Best Local Similarity 88.1%; Pred. No. 1.7e-134;
Matches 406; Conservative 18; Mismatches 22; Indels 15; Gaps 1;
QY 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYRMHWVRQAPGQGLEWIGYINPSTGVTEY 60
DB 20 QVQLVQSGAEVKKPGSSVKVSCKASGSGFVISWRQAPGQGLAWGIIIPAFDITKY 79
QY 61 NQKFKDKATITADESTNTAYMELSLRSEDYAVYCAARGGVF-----DY 105
DB 80 AQNFQDRTVTSADESDTAYMELSLRSEDYAVYCARDLALYELWSGFHTDEKYYGLDV 139
QY 106 WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 165
DB 140 WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 199
QY 166 VHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHPKSNITKVDKVEPKSCDKTHTC 225
DB 200 VHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHPKSNITKVDKVEPKSCDKTHTC 259
QY 226 PPCPAPELLGGPSVFLFPPKPKDQXMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 285
DB 260 PPCPAPELLGGPSVFLFPPKPKDQXMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 319
QY 286 AKTAPREEQYNSTYRVSVLVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREP 345
DB 320 AKTAPREEQYNSTYRVSVLVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREP 379
QY 346 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFL 405
DB 380 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFL 439
QY 406 YSKLTVDKSRWQQGNVFCVSVLXALHNHYTQKSLSLSPGK 446
DB 440 YSKLTVDKSRWQQGNVFCVSVLXALHNHYTQKSLSLSPGK 480
RESULT 3
Q6N095_HUMAN PRELIMINARY; PRT; 475 AA.
ID Q6N095_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6N095;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686K03196.
GN Name=DKFZp686K03196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;